1

SEQUENCE LISTINGS

<110> INJE UNIVERSITY

<120> CANCER CELL TARGETING GENE DELIVERY METHOD

<130> PCA31275/IJU

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<223> 597LN primer

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2

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3

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<223>   surface subunit region

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<222>   (1468)..(2025)
<223>   transmembrain domain

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gggacgagtc tgcaaaataa gaaccccac cagcccatga ccctcacttg gcaggtactg   180

tcccaaactg gagacgttgt ctgggataca aaggcagtcc agccccttg gacttggtgg   240

cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg   300

ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct   360

tataagcaaa tcacctgggg agccataggg tgcagctacc ctcgggctag gactagaatg   420

gcaagctcta ccttctacgt atgtccccgg gatggccgga ccctttcaga agctagaagg   480

tgcggggggc tagaatccct atactgtaaa gaatgggatt gtgagaccac ggggaccggt   540

tattggctat ctaaatcctc aaaagacctc ataactgtaa aatgggacca aaatagcgaa   600

4

tggactcaaa aatttcaaca gtgtcaccag accggctggt gtaaccccct taaaatagat   660

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ttctatgtgt ctggacatcc aggcgtacag ttcaccattc gcttaaaaat caccaacatg   780

ccagctgtgg cagtaggtcc tgacctcgtc cttgtggaac aaggacctcc tagaacgtcc   840

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aattcctccg gagaccatca gtatctgctc ccctccaacc atagctggtg ggcttgcagc   1320

actggcctca ccccttgcct ctccacctca gttttttaatc agactagaga tttctgtatc   1380

caggtccagc tgattcctcg catctattac tatcctgaag aagtttttgtt acaggcctat   1440

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aataggagag gccttgactt gctgtttcta aaagaaggtg gcctctgtgc ggccctaaag   1740

gaagagtgct gttttttacat agaccactca ggtgcagtac gggactccat gaaaaaactc   1800

aaagaaaaac tggataaaag acagttagag cgccagaaaa gccaaaactg gtatgaagga   1860

tggttcaata actcccccttg gttcactacc ctgctatcaa ccatcgctgg gcccctatta   1920

5

ctcctccttc	tgttgctcat	cctcgggcca	tgcatcatca	ataagttagt	tcaattcatc	1980
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aacgaaggta	accttttaa					2058

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<213>    Tag-72pS1

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<223>    (Gly4Ser)3 linker

<220>
<221>    misc_feature
<222>    (739)..(777)
<223>    PreS1 Tag

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6

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agcgggtctg ggacagattt cactctcacc atcagcagcc tgcaggctga agatgtggca   660

gtttattact gtcagcaata ttattcctat ccgttgacgt tcggccaagg gaccaaggtg   720

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gcatag   786

<210>   9
<211>   13
<212>   PRT
<213>   PreS1 epitope at C-terminal of Tag-72pS1

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<210>   10
<211>   2871
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA

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gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg   180

tcccaaactg gagacgttgt ctgggataca aaggcagtcc agccccccttg gacttggtgg   240

cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg   300

ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct   360

tataagcaaa tcacctgggg agccataggg tgcagctacc ctcgggctag gactagaatg   420

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gcaagatcgt tgaacatggc atactggggc caagggactc tggtcactgt ctcttcaggt   960

ggaggcggtt caggcggagg tggctctggc ggtggcggat cggacattgt gatgacccag   .1020

tctccagact ccctggctgt gtctctgggc gagagggcca ccatcaactg caagtccagc   1080

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gactggataa cgggaaaaac ctggggatta agattctatg tgtctggaca tccaggcgta   1560

cagttcacca ttcgcttaaa aatcaccaac atgccagctg tggcagtagg tcctgacctc   1620

gtccttgtgg aacaaggacc tcctagaacg tccctcgctc tcccacctcc tcttcccca   1680

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8

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aagctcaccc tcactgaggt ctcaggacac gggttgtgca taggaaaggt gccctttacc    2040

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ctcccctcca accatagctg gtgggcttgc agcactggcc tcaccccttg cctctccacc    2160

tcagttttta atcagactag agatttctgt atccaggtcc agctgattcc tcgcatctat    2220

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gaggctgtct cacttaccct agctgtttta ctggggttgg gaatcacggc gggaataggt    2340

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cagatcgcca tagatgctga cctccgggcc ctccaagact cagtcagcaa gttagaggac    2460

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gagcgccaga aaagccaaaa ctggtatgaa ggatggttca ataactcccc ttggttcact    2700

accctgctat caaccatcgc tgggcccctc ttactcctcc ttctgttgct catcctcggg    2760

ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaaatt    2820

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<210> 11
<211> 956
<212> PRT
<213> Artificial Sequence

9

<220>
<223>   ScFv-GaLV Env GP chimeric ligand (FvGEL199)

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Met Val Leu Leu Pro Gly Ser Met Leu Leu Thr Ser Asn Leu His His
 1   5   10   15

Leu Arg His Gln Met Ser Pro Gly Ser Trp Lys Arg Leu Ile Ile Leu
           20   25   30

Leu Ser Cys Val Phe Gly Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
         35   40   45

Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
     50   55   60

Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp
65   70   75   80

Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser
             85   90   95

Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro
         100   105   110

Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala
         115   120   125

Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr
     130   135   140

Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg
145   150   155   160

Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr
             165   170   175

Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr
             180   185   190

Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
         195   200   205

10

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
    210   215   220

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp
225   230   235   240

Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp Met Gly Tyr Phe Ser
            245   250   255

Pro Gly Asn Asp Asp Phe Lys Tyr Ser Gln Lys Phe Gln Gly Arg Val
            260   265   270

Thr Ile Thr Ala Asp Lys Ser Ala Ser Thr Ala Tyr Met Glu Leu Ser
    275   280   285

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Leu
    290   295   300

Asp Met Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
305   310   315   320

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
            325   330   335

Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg
            340   345   350

Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn
    355   360   365

Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
    370   375   380

Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp
385   390   395   400

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
            405   410   415

Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr
            420   425   430

Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Ala

11

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        435                 440                 445

Ala Ala Gly Ala Asn Ala Asn Asn Pro Asp Trp Asp Phe Asn Pro Ala
    450                 455                 460

Ala Gly Gly Gly Gly Ser Glu Trp Thr Gln Lys Phe Gln Gln Cys His
465                 470                 475                 480

Gln Thr Gly Trp Cys Asn Pro Leu Lys Ile Asp Phe Thr Asp Lys Gly
                485                 490                 495

Lys Leu Ser Lys Asp Trp Ile Thr Gly Lys Thr Trp Gly Leu Arg Phe
            500                 505                 510

Tyr Val Ser Gly His Pro Gly Val Gln Phe Thr Ile Arg Leu Lys Ile
        515                 520                 525

Thr Asn Met Pro Ala Val Ala Val Gly Pro Asp Leu Val Leu Val Glu
    530                 535                 540

Gln Gly Pro Pro Arg Thr Ser Leu Ala Leu Pro Pro Pro Leu Pro Pro
545                 550                 555                 560

Arg Glu Ala Pro Pro Pro Ser Leu Pro Asp Ser Asn Ser Thr Ala Leu
                565                 570                 575

Ala Thr Ser Ala Gln Thr Pro Thr Val Arg Lys Thr Ile Val Thr Leu
            580                 585                 590

Asn Thr Pro Pro Pro Thr Thr Gly Asp Arg Leu Phe Asp Leu Val Gln
            595                 600                 605

Gly Ala Phe Leu Thr Leu Asn Ala Thr Asn Pro Gly Ala Thr Glu Ser
    610                 615                 620

Cys Trp Leu Cys Leu Ala Met Gly Pro Pro Tyr Tyr Glu Ala Ile Ala
625                 630                 635                 640

Ser Ser Gly Glu Val Ala Tyr Ser Thr Asp Leu Asp Arg Cys Arg Trp
                645                 650                 655

Gly Thr Gln Gly Lys Leu Thr Leu Thr Glu Val Ser Gly His Gly Leu
            660                 665                 670
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12

Cys Ile Gly Lys Val Pro Phe Thr His Gln His Leu Cys Asn Gln Thr
        675   680   685

Leu Ser Ile Asn Ser Ser Gly Asp His Gln Tyr Leu Leu Pro Ser Asn
    690   695   700

His Ser Trp Trp Ala Cys Ser Thr Gly Leu Thr Pro Cys Leu Ser Thr
705   710   715   720

Ser Val Phe Asn Gln Thr Arg Asp Phe Cys Ile Gln Val Gln Leu Ile
            725   730   735

Pro Arg Ile Tyr Tyr Tyr Pro Glu Glu Val Leu Leu Gln Ala Tyr Asp
            740   745   750

Asn Ser His Pro Arg Thr Lys Arg Glu Ala Val Ser Leu Thr Leu Ala
        755   760   765

Val Leu Leu Gly Leu Gly Ile Thr Ala Gly Ile Gly Thr Gly Ser Thr
    770   775   780

Ala Leu Ile Lys Gly Pro Ile Asp Leu Gln Gln Gly Leu Thr Ser Leu
785   790   795   800

Gln Ile Ala Ile Asp Ala Asp Leu Arg Ala Leu Gln Asp Ser Val Ser
            805   810   815

Lys Leu Glu Asp Ser Leu Thr Ser Leu Ser Glu Val Val Leu Gln Asn
        820   825   830

Arg Arg Gly Leu Asp Leu Leu Phe Leu Lys Glu Gly Gly Leu Cys Ala
        835   840   845

Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ile Asp His Ser Gly Ala Val
    850   855   860

Arg Asp Ser Met Lys Lys Leu Lys Glu Lys Leu Asp Lys Arg Gln Leu
865   870   875   880

Glu Arg Gln Lys Ser Gln Asn Trp Tyr Glu Gly Trp Phe Asn Asn Ser
            885   890   895

Pro Trp Phe Thr Thr Leu Leu Ser Thr Ile Ala Gly Pro Leu Leu Leu
        900   905   910

13

Leu Leu Leu Leu Leu Ile Leu Gly Pro Cys Ile Ile Asn Lys Leu Val
        915   920   925

Gln Phe Ile Asn Asp Arg Ile Ser Ala Val Lys Ile Leu Val Leu Arg
    930   935   940

Gln Lys Tyr Gln Ala Leu Glu Asn Glu Gly Asn Leu
945   950   955